AMENDMENTS TO THE SPECIFICATION:

Please replace paragraph [0046] with the following paragraph:

[0046] With the help of the Pfam database (Batemann et al., 2002, Nucleic Acids Research 30, 276-280; accessible via ~~http://www.sanger.ac.uk/Software/Pfam/, http://www.cgb.ki.se/Pfam/; http://pfam.jouy.inra.fr/ or http://pfam.wustl.edu/)~~ the Wellcome Trust Sanger Institute website or the Institute National de la Recherche Agronomique website)), it is possible for the person skilled in the art to determine whether amino acid sequences already have known domains (e.g. an iso-amylase domain and/or an alpha-amylase domain). Pfam is a database put together by experts, which classifies amino acid sequences into so-called families. Here, the assignment of an amino acid sequence to a family is carried out on the basis of so-called domains, which are to be looked upon as functional and structural components of proteins. A domain is defined as a structural unit or a repeatedly occurring amino acid sequence unit, which can occur in proteins with widely different functions. Along with information relating to the amino acid sequence of known proteins, further knowledge (e.g. evidence of the enzymatic activity, crystal structure data) is also used for the assignment of a protein to a family. Each family is assigned a name and an "accession" number (e.g. Name: Isoamylase_N, acc: PF02922). A constituent part of each family in the Pfam database is, amongst other things, a so-called "seed alignment". The "seed alignment" contains the amino acid sequences of representative proteins of a family. Starting from "seed alignments", a so-called profile HMM ("profile Hidden Markov Model"; overview article in: Durbin et al., "Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids", Cambridge University Press, 1998, ISBN 0-521-62041-4) is produced using the HMMER 2 software (freely available ~~under http://hmmer.wustl.edu/~~ on the world wide web). The HMMs produced have names and are stored in the Pfam database specifically for the correspondingly assigned domains. In contrast to classical, multiple "alignments" (e.g. produced using the Clustal W program or the Blossum62 algorithm), HMMs are based on a valid statistical theory (Bayes theory of conditional probability, Markoff chains) and enable an interrogation sequence (query) to be assigned to a family based on the use of position-specific evaluation matrices. This enables an assignment to be made even when there are considerable differences in the amino acid sequences between the

interrogation sequence (query) and a comparison sequence (e.g. amino acid sequence entry in a database).

Please replace paragraph [0047] with the following paragraph:

[0047] The domain structure of the amino acid sequence concerned can be determined by means of a comparison of the HMMs stored in the Pfam database with amino acid sequences, which are entered as a so-called interrogation sequence (query) (e.g. ~~under http://hits.isb-sib.ch/cgi-bin/PFSCAN?~~ myhits motif scan, available on the world wide web).

Please replace paragraph [0049] with the following paragraph:

[0049] In conjunction with the present invention, the term "alpha-amylase domain" is to be understood to mean a Pfam alpha-amylase domain (acc: Pf00128). At the same time, the HMM describing this Pfam alpha-amylase domain is to be produced with the HMMER 2 [2.3.1] software, starting from a "seed alignment", which contains the amino acid sequences shown in Table 2. Here, the "seed alignment" is produced by means of HMM_simulated_annealing ~~(http://www.psc.edu/general/software/packages/hmmer/manual/node11.html#SECTION00321000000000000000~~ available on the world wide web). The following settings must be chosen to produce the appropriate HMM: Build Method of HMM: hmmbuild-F HMM_Is, hmmcalibrate-seed 0 HMM_Is; Gathering cutoff: -82.0-82.0; Trusted cutoff: -81.7-81.7; Noise cutoff: -82.7-82.7). Further information for producing the HMM of the Pfam alpha-amylase domain (acc: Pf00128) is given in Table 4.

Please replace the following paragraphs after paragraph [00265]:

Description of the Figures

FIG. 1 ~~Table 1~~ shows the amino acid sequences, contained in the "seed alignment," that are used for producing the HMM describing for the Pfam isoamylase domain (PF 02922).

FIG. 2 ~~Table 2~~ shows the amino acid sequences, contained in the "seed alignment," that are used for producing the HMM describing for the Pfam alpha-amylase domain (PF 00128).

FIGS. 3-11 ~~Table 3~~ show information for producing the HMM for the Pfam isoamylase domain (PF 02922).

FIGS. 12-43 ~~Table 4~~ show information for producing the HMM for the Pfam alpha-amylase domain (PF 00128).